Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in this application:

Claims 1-126 (cancelled).

Claim 127 (previously presented). A method for identifying an aptamer regulator comprising the steps:

a) providing a target and a target partner that do not bind to each other in the absence of an aptamer regulator;

b) contacting a mixture of nucleic acids with the target and the target partner under conditions that disfavor efficient binding between the target and the target partner;

c) partitioning nucleic acids bound to a target-target partner complex from unbound nucleic acids; and

d) retaining the nucleic acids bound to the target-target partner complex,

thereby identifying an aptamer regulator that binds to a target wherein binding of the aptamer regulator to the target increases the binding affinity of the target for the target partner relative to the affinity of the target for the target partner when the target is not bound by the aptamer regulator such that binding of the aptamer regulator to the target is a prerequisite for target-target partner complex formation.

Claim 128 (previously presented). The method of claim 127, wherein the mixture of nucleic acids is a target-specific pool of nucleic acids having high affinity and specificity for the target.

Claim 129 (previously presented). The method of claim 128, wherein the target-specific pool of nucleic acids is diversified.

Claim 130 (previously presented). The method of claim 127, wherein the target partner is immobilized.

Claim 131 (previously presented). The method of claim 127, wherein the method further comprises a negative selection prior to step a).

Claim 132 (previously presented). The method of claim 131, wherein the negative selection comprises the steps:

1) contacting a mixture of nucleic acids with the target partner under conditions that favor specific binding between the nucleic acids and the target partner; and

2) partitioning the bound nucleic acids from the unbound nucleic acids, and retaining the unbound nucleic acids;

wherein the unbound nucleic acids are then contacted with the target and the target partner in step b).

Claim 133 (previously presented). The method of claim 127, wherein the method further comprises the step of removing the retained nucleic acids from the target-target partner complex.

Claim 134 (previously presented). The method of claim 133, wherein the removing is by eluting the nucleic acids with an agonist competitor to the target.

Claim 135 (previously presented). The method of claim 133, wherein the removing is by contacting the bound nucleic acids with excess free target.

Claim 136 (previously presented). The method of claim 127, wherein the method further comprises the step of amplifying the retained nucleic acids and repeating steps a) to d).

Claim 137 (previously presented). The method of claim 127, wherein the method further comprises the step of screening the nucleic acids retained in step d) for a desired functional activity.